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RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/697,863A

DATE: 08/21/2002

TIME: 15:13:47

Input Set : A:\2676-4555 seq listing v2.ST25.txt
 Output Set: N:\CRF4\08212002\I697863A.raw

Don Lefever
1600
WV/PLB

3 <110> APPLICANT: Vlaams Interuniversitair Instituut Voor Biotechnologie VZW
 5 <120> TITLE OF INVENTION: CD-40 INTERACTING AND TRAF-INTERACTING PROTEINS
 7 <130> FILE REFERENCE: 2676-4555US
 9 <140> CURRENT APPLICATION NUMBER: US 09/697,863A
 10 <141> CURRENT FILING DATE: 2000-10-27
 12 <150> PRIOR APPLICATION NUMBER: PCT/EP99/03025
 13 <151> PRIOR FILING DATE: 1999-04-28
 15 <150> PRIOR APPLICATION NUMBER: EPO 98201392.2
 16 <151> PRIOR FILING DATE: 1998-04-29
 18 <160> NUMBER OF SEQ ID NOS: 6
 20 <170> SOFTWARE: PatentIn version 3.1
 22 <210> SEQ ID NO: 1
 23 <211> LENGTH: 1920
 24 <212> TYPE: DNA
 25 <213> ORGANISM: Homo sapiens
 27 <220> FEATURE:
 28 <221> NAME/KEY: misc_feature
 29 <222> LOCATION: (1627)..(1627)
 30 <223> OTHER INFORMATION: N stands for any nucleotide.
 33 <220> FEATURE:
 34 <221> NAME/KEY: CDS
 35 <222> LOCATION: (20)..(1108)
 36 <223> OTHER INFORMATION:
 38 <220> FEATURE:
 39 <221> NAME/KEY: misc_feature
 40 <222> LOCATION: (1849)..(1849)
 41 <223> OTHER INFORMATION: N stands for any nucleotide.
 44 <400> SEQUENCE: 1
 45 gtgcagaggc ggcaggaag atg gag ttg ggg agt tgc ctg gag ggc ggg agg 52
 46 Met Glu Leu Gly Ser Cys Leu Glu Gly Gly Arg
 47 1 5 10
 49 gag gcg gcg gag gaa gag ggc gag cct gag gtg aaa aag cgg cga ctt 100
 50 Glu Ala Ala Glu Glu Gly Glu Pro Glu Val Lys Lys Arg Arg Leu
 51 15 20 25
 53 ctg tgt gtg gag ttt gcc tcg gtc gca agc tgc gat gcc gca gtg gct 148
 54 Leu Cys Val Glu Phe Ala Ser Val Ala Ser Cys Asp Ala Ala Val Ala
 55 30 35 40
 57 cag tgc ttc ctg gcc gag aac gac tgg gag atg gaa agg gct ctg aac 196
 58 Gln Cys Phe Leu Ala Glu Asn Asp Trp Glu Met Glu Arg Ala Leu Asn
 59 45 50 55
 61 tcc tac ttc gag cct ccg gtg gag gag agc gcc ttg gaa cgc cga cct 244
 62 Ser Tyr Phe Glu Pro Pro Val Glu Glu Ser Ala Leu Glu Arg Arg Pro
 63 60 65 70 75

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65	gaa acc atc tct gag ccc aag acc tat gtt gac cta acc aat gaa gaa	292
66	Glu Thr Ile Ser Glu Pro Lys Thr Tyr Val Asp Leu Thr Asn Glu Glu	
67	80 85 90	
69	aca act gat tcc acc act tct aaa atc agc cca tct gaa gat act cag	340
70	Thr Thr Asp Ser Thr Ser Lys Ile Ser Pro Ser Glu Asp Thr Gln	
71	95 100 105	
73	caa gaa aat ggc agc atg ttc tct ctc att acc tgg aat att gat gga	388
74	Gln Glu Asn Gly Ser Met Phe Ser Leu Ile Thr Trp Asn Ile Asp Gly	
75	110 115 120	
77	tta gat cta aac aat ctg tca gag agg gct cga ggg gtg tgt tcc tac	436
78	Leu Asp Leu Asn Asn Leu Ser Glu Arg Ala Arg Gly Val Cys Ser Tyr	
79	125 130 135	
81	tta gct ttg tac agc cca gat gtg ata ttt cta cag gaa gtt att ccc	484
82	Leu Ala Leu Tyr Ser Pro Asp Val Ile Phe Leu Gln Glu Val Ile Pro	
83	140 145 150 155	
85	cca tat tat agc tac cta aag aag aga tca agt aat tat gag att att	532
86	Pro Tyr Tyr Ser Tyr Leu Lys Lys Arg Ser Ser Asn Tyr Glu Ile Ile	
87	160 165 170	
89	aca ggt cat gaa gaa gga tat ttc aca gct ata atg ttg aag aaa tca	580
90	Thr Gly His Glu Glu Gly Tyr Phe Thr Ala Ile Met Leu Lys Ser	
91	175 180 185	
93	aga gtg aaa tta aaa agc caa gag att att cct ttt cca agt acc aaa	628
94	Arg Val Lys Leu Lys Ser Gln Glu Ile Ile Pro Phe Pro Ser Thr Lys	
95	190 195 200	
97	atg atg aga aac ctt tta tgt gtg cat gtg aat gtg tca gga aat gag	676
98	Met Met Arg Asn Leu Leu Cys Val His Val Asn Val Ser Gly Asn Glu	
99	205 210 215	
101	ctt tgc ctt atg aca tcc cat ttg gag agc acc aga ggg cat gct gcg	724
102	Leu Cys Leu Met Thr Ser His Leu Glu Ser Thr Arg Gly His Ala Ala	
103	220 225 230 235	
105	gaa cga atg aat cag tta aaa atg gtt tta aag aaa atg caa gag gct	772
106	Glu Arg Met Asn Gln Leu Lys Met Val Leu Lys Lys Met Gln Glu Ala	
107	240 245 250	
109	cca gag tca gct aca gtt ata ttt gca gga gat aca aat cta agg gat	820
110	Pro Glu Ser Ala Thr Val Ile Phe Ala Gly Asp Thr Asn Leu Arg Asp	
111	255 260 265	
113	cga gag gtt acc aga tgt ggt ggt tta ccc aac aac att gtg gat gtc	868
114	Arg Glu Val Thr Arg Cys Gly Gly Leu Pro Asn Asn Ile Val Asp Val	
115	270 275 280	
117	tgg gag ttt ttg ggc aaa cct aaa cat tgc cag tat aca tgg gat aca	916
118	Trp Glu Phe Leu Gly Lys Pro Lys His Cys Gln Tyr Thr Trp Asp Thr	
119	285 290 295	
121	caa atg aac tct aat ctt gga ata act gct gct tgt aaa ctt cgt ttt	964
122	Gln Met Asn Ser Asn Leu Gly Ile Thr Ala Ala Cys Lys Leu Arg Phe	
123	300 305 310 315	
125	gat cga ata ttt ttc aga gca gca gaa gag gga cac att att ccc	1012
126	Asp Arg Ile Phe Phe Arg Ala Ala Glu Glu Gly His Ile Ile Pro	
127	320 325 330	
129	cga agt ttg gac ctt ctt gga aat ctg gac tgt ggt aga ttt	1060

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130	Arg	Ser	Leu	Asp	Leu	Leu	Gly	Leu	Glu	Lys	Leu	Asp	Cys	Gly	Arg	Phe	
131				335				340						345			
133	cct	agt	gat	cac	tgg	ggt	ctt	ctg	tgc	aac	tta	gat	ata	ata	ttg	taa	1108
134	Pro	Ser	Asp	His	Trp	Gly	Leu	Leu	Cys	Asn	Leu	Asp	Ile	Ile	Leu		
135				350				355						360			
137	aatgctttc	aagtgtgggt	tttgccctga	ttgttgcaaa	tacaatttcc	accttctgga										1168	
139	aaggtaggtt	tgctgtggag	gaaataatgt	actagatcat	tgtcacagaaa	aaacccaacta										1228	
141	tgatttatgg	ttgtgttttc	agaattcaac	attaaagatt	aatgtttatt	taaacgaaca										1288	
143	cattcctgca	ttcaggatgt	gaggccattt	aataaaaagg	gcacaaagcc	tgtcagagtt										1348	
145	ttcaacggtg	cttacagctg	ccagctgat	tccaaacagg	taccccattt	tctctgagct										1408	
147	aatgtttata	ttttccatt	cagggcaccga	aatagttaat	atttaaaata	agtcttcaaa										1468	
149	agaaaaacata	agagattatt	gagttctgg	gactggatcc	tttatttcat	aagttcagat										1528	
151	catcttaaat	gaaaatgcca	tgattatctg	cagttaaat	gatgacagct	attctacatc										1588	
W-->	153	agacttgatt	tttgtcagct	aattacataa	ttggtaagnt	ataattgaaa	ccttatggct									1648	
155	taaaaattcct	taactcctt	ttgattcatg	tttgttagtca	tgttgtcaac	agaggcaaaag										1708	
157	ttaagcttga	tgatggtaa	aatcggtttg	atagcaccat	gggacatttt	tttaacaaaa										1768	
159	ataaaatgcat	gaagagacat	agccttttag	ttttgctaatt	tgtgaaatgg	aaatgcttta										1828	
W-->	161	caggaagtaa	atgcaaatta	nttttaagtg	tgctttaag	aaaaatattt	tccccacagg									1888	
163	agaaaatttaa	ataaagaatt	ttatttggta	aa												1920	
166	<210>	SEQ ID NO:	2														
167	<211>	LENGTH:	362														
168	<212>	TYPE:	PRT														
169	<213>	ORGANISM:	Homo sapiens														
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174	1				5			10			15						
177	Glu	Gly	Glu	Pro	Glu	Val	Lys	Lys	Arg	Arg	Leu	Leu	Cys	Val	Glu	Phe	
178					20			25			30						
181	Ala	Ser	Val	Ala	Ser	Cys	Asp	Ala	Ala	Val	Ala	Gln	Cys	Phe	Leu	Ala	
182					35			40			45						
185	Glu	Asn	Asp	Trp	Glu	Met	Glu	Arg	Ala	Leu	Asn	Ser	Tyr	Phe	Glu	Pro	
186					50			55			60						
189	Pro	Val	Glu	Glu	Ser	Ala	Leu	Glu	Arg	Arg	Pro	Glu	Thr	Ile	Ser	Glu	
190	65				70			75			80						
193	Pro	Lys	Thr	Tyr	Val	Asp	Leu	Thr	Asn	Glu	Glu	Thr	Thr	Asp	Ser	Thr	
194					85			90			95						
197	Thr	Ser	Lys	Ile	Ser	Pro	Ser	Glu	Asp	Thr	Gln	Gln	Glu	Asn	Gly	Ser	
198					100			105			110						
201	Met	Phe	Ser	Leu	Ile	Thr	Trp	Asn	Ile	Asp	Gly	Leu	Asp	Leu	Asn	Asn	
202					115			120			125						
205	Leu	Ser	Glu	Arg	Ala	Arg	Gly	Val	Cys	Ser	Tyr	Leu	Ala	Leu	Tyr	Ser	
206					130			135			140						
209	Pro	Asp	Val	Ile	Phe	Leu	Gln	Glu	Val	Ile	Pro	Pro	Tyr	Tyr	Ser	Tyr	
210	145				150			155			160						
213	Leu	Lys	Lys	Arg	Ser	Ser	Asn	Tyr	Glu	Ile	Ile	Thr	Gly	His	Glu	Glu	
214					165			170			175						
217	Gly	Tyr	Phe	Thr	Ala	Ile	Met	Leu	Lys	Lys	Ser	Arg	Val	Lys	Leu	Lys	
218					180			185			190						
221	Ser	Gln	Glu	Ile	Ile	Pro	Phe	Pro	Ser	Thr	Lys	Met	Met	Arg	Asn	Leu	

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222	195	200	205	
225	Leu Cys Val His Val Asn Val Ser Gly Asn Glu Leu Cys Leu Met Thr			
226	210	215	220	
229	Ser His Leu Glu Ser Thr Arg Gly His Ala Ala Glu Arg Met Asn Gln			
230	225	230	235	240
233	Leu Lys Met Val Leu Lys Lys Met Gln Glu Ala Pro Glu Ser Ala Thr			
234	245	250	255	
237	Val Ile Phe Ala Gly Asp Thr Asn Leu Arg Asp Arg Glu Val Thr Arg			
238	260	265	270	
241	Cys Gly Gly Leu Pro Asn Asn Ile Val Asp Val Trp Glu Phe Leu Gly			
242	275	280	285	
245	Lys Pro Lys His Cys Gln Tyr Thr Trp Asp Thr Gln Met Asn Ser Asn			
246	290	295	300	
249	Leu Gly Ile Thr Ala Ala Cys Lys Leu Arg Phe Asp Arg Ile Phe Phe			
250	305	310	315	320
253	Arg Ala Ala Ala Glu Glu Gly His Ile Ile Pro Arg Ser Leu Asp Leu			
254	325	330	335	
257	Leu Gly Leu Glu Lys Leu Asp Cys Gly Arg Phe Pro Ser Asp His Trp			
258	340	345	350	
261	Gly Leu Leu Cys Asn Leu Asp Ile Ile Leu			
262	355	360		
265	<210> SEQ ID NO: 3			
266	<211> LENGTH: 1312			
267	<212> TYPE: DNA			
268	<213> ORGANISM: Mus musculus			
270	<220> FEATURE:			
271	<221> NAME/KEY: CDS			
272	<222> LOCATION: (122)..(1234)			
273	<223> OTHER INFORMATION:			
275	<400> SEQUENCE: 3			
276	agctattaaat gattcgaatt tatacgactc actataggga atttggccct cgaggccaag	60		
278	aattcggcac gagggcgaaa agcagcgtga agagcggtg ttttgggggg accctgcggc	120		
280	g atg gcg tct ggc agc agt tcc gat gcg gcg gag ccc gca ggg ccg gca	169		
281	Met Ala Ser Gly Ser Ser Asp Ala Ala Glu Pro Ala Gly Pro Ala			
282	1 5 10 15			
284	ggg cgg gcg tcg gcg ccc gaa gca gca cag gcg gag gag gac cgg	217		
285	Gly Arg Ala Ala Ser Ala Pro Glu Ala Ala Gln Ala Glu Glu Asp Arg			
286	20 25 30			
288	gtg aag agg cgg cgg ctt cag tgc ctg ggc ttt gcg ttg gtg ggg gga	265		
289	Val Lys Arg Arg Leu Gln Cys Leu Gly Phe Ala Leu Val Gly Gly			
290	35 40 45			
292	tgc gac ccc acg atg gtc ccc agc gtc ctg cgg gag aac gac tgg cag	313		
293	Cys Asp Pro Thr Met Val Pro Ser Val Leu Arg Glu Asn Asp Trp Gln			
294	50 55 60			
296	acg cag aaa gcc ctg agc gcc tac ttc gag ctg cca gag aac gac caa	361		
297	Thr Gln Lys Ala Leu Ser Ala Tyr Phe Glu Leu Pro Glu Asn Asp Gln			
298	65 70 75 80			
300	ggg tgg ccc cgc cag cct ccc acg tcc ttc aag tcc gag gcc tat gtt	409		
301	Gly Trp Pro Arg Gln Pro Pro Thr Ser Phe Lys Ser Glu Ala Tyr Val			

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302	85	90	95	
304	gat cta acc aac gag gat gca aat gat aca acc att tta gaa gcc agt			457
305	Asp Leu Thr Asn Glu Asp Ala Asn Asp Thr Thr Ile Leu Glu Ala Ser			
306	100	105	110	
308	cca tct gga act cct cta gaa gat agc agc act att tct ttc att acc			505
309	Pro Ser Gly Thr Pro Leu Glu Asp Ser Ser Thr Ile Ser Phe Ile Thr			
310	115	120	125	
312	tgg aat att gat gga tta gat gga tgc aat ctg ccc gag agg gct cga			553
313	Trp Asn Ile Asp Gly Leu Asp Gly Cys Asn Leu Pro Glu Arg Ala Arg			
314	130	135	140	
316	ggg gtg tgt tcc tgc cta gct ttg tat agt cca gat gtg gta ttt cta			601
317	Gly Val Cys Ser Cys Leu Ala Leu Tyr Ser Pro Asp Val Val Phe Leu			
318	145	150	155	160
320	cag gaa gtt atc ccc cca tac tgt gcc tac cta aag aag aga gca gcc			649
321	Gln Glu Val Ile Pro Pro Tyr Cys Ala Tyr Leu Lys Lys Arg Ala Ala			
322	165	170	175	
324	agt tac aca att att aca ggt aat gaa gaa gga tat ttc aca gct ata			697
325	Ser Tyr Thr Ile Ile Thr Gly Asn Glu Glu Gly Tyr Phe Thr Ala Ile			
326	180	185	190	
328	cta ttg aag aaa gga aga gtc aaa ttt aaa agt cag gag att att cct			745
329	Leu Leu Lys Lys Gly Arg Val Lys Phe Lys Ser Gln Glu Ile Ile Pro			
330	195	200	205	
332	ttt cca aat acc aaa atg aga aac ctg cta tgc gta aat gtg agt			793
333	Phe Pro Asn Thr Lys Met Met Arg Asn Leu Leu Cys Val Asn Val Ser			
334	210	215	220	
336	ttg ggt gga aat gaa ttt tgc ott atg aca tcc cat ttg gag agc acc			841
337	Leu Gly Gly Asn Glu Phe Cys Leu Met Thr Ser His Leu Glu Ser Thr			
338	225	230	235	240
340	aga gaa cat tct gcg gaa cga ata aga caa tta aaa act gtt ctt gga			889
341	Arg Glu His Ser Ala Glu Arg Ile Arg Gln Leu Lys Thr Val Leu Gly			
342	245	250	255	
344	aaa atg caa gag gct cca gat tca acc acg gtt ata ttt gca gga gat			937
345	Lys Met Gln Glu Ala Pro Asp Ser Thr Thr Val Ile Phe Ala Gly Asp			
346	260	265	270	
348	aca aat tta aga gat caa gaa gtt atc aaa tgt ggt ggt tta cct gac			985
349	Thr Asn Leu Arg Asp Gln Glu Val Ile Lys Cys Gly Leu Pro Asp			
350	275	280	285	
352	aac gtt ttt gat gcc tgg gaa ttt tta ggc aaa cct aaa cat tgc cag			1033
353	Asn Val Phe Asp Ala Trp Glu Phe Leu Gly Lys Pro Lys His Cys Gln			
354	290	295	300	
356	tat aca tgg gat acg aaa gca aat aac aac ctc agg atc cct gct gct			1081
357	Tyr Thr Trp Asp Thr Lys Ala Asn Asn Asn Leu Arg Ile Pro Ala Ala			
358	305	310	315	320
360	tat aag cat cgt ttt gat cga ata ttt ttc aga gca gaa gag ggg cac			1129
361	Tyr Lys His Arg Phe Asp Arg Ile Phe Phe Arg Ala Glu Glu Gly His			
362	325	330	335	
364	ctt att cct caa agt tta gac ctt gtt ggg ttg gaa aaa ctg gac tgt			1177
365	Leu Ile Pro Gln Ser Leu Asp Leu Val Gly Leu Glu Lys Leu Asp Cys			
366	340	345	350	

RAW SEQUENCE LISTING ERROR SUMMARY DATE: 08/21/2002
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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:1; N Pos. 1627,1849
Seq#:5; N Pos. 1392,1530,1531
Seq#:5; Xaa Pos. 395,441
Seq#:6; Xaa Pos. 395,441

VERIFICATION SUMMARY
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L:153 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1 after pos.:1588
L:161 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1 after pos.:1828
L:611 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5 after pos.:1384
L:612 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5 after pos.:1432
L:623 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5 after pos.:1528
L:624 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5 after pos.:1536
L:742 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6 after pos.:384
L:754 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6 after pos.:432